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# The impact of information technology in biological sciences

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## Abstract

The advent of computer and information technology thereafter has been making such conspicuously remarkable changes in every aspect of life that its importance cannot be over accentuated. Biological sciences are not an exception in the profit made from IT. This study aims to investigate the impact of information technology in biological sciences. The descriptive library based research showed that information technology played three following impacts in biological sciences: IT makes a great revolution in remote education; IT leads to a remarkable improvement in biological simulation and modeling; and last but not least Information Technology makes a visible in laboratory studies.

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## 1. Introduction

Computer and internet play the most conspicuous roles in all aspects of human life. Computer related technologies have a strong impact on the world. These have attracted many students and professionals to the field of information technology. There are thousands of web sites and web hosting opportunities available which are ever growing. Many information technologies, from the earliest computers to email and the Internet, have been developed for scientific applications.

As Cheney (2003) states: “Understanding the role of IT for science is important because of the central role of science in today’s information society. Advances in science affect economic performance and the achievement of societal goals, from health to national security. As a result, it is important for policy makers to understand how IT affects the quality and productivity of science.

It can be understood from the observation and the literature that there are several complementary approaches to examining the implications of IT for science. One approach is to examine the role of specific information technologies, such as email or the World Wide Web. Another approach is to examine the role of IT in specific aspects of the scientific process, such as scholarly communication or scientific collaboration. In this study, the implementations of IT are elaborated. Biology is at its core an informational science based on the information embedded in the genetic code. At the molecular level, a key challenge in biology is to understand how instructions encoded in genomes lead to the structure and function of the proteins, and the regulation and expression of genes. IT

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is essential to store, manage, and decipher the mass of information produced in work in these areas. At levels of organization above the molecular level, computer models are critical tools to handle the complexity of relationships in biology.

It is shown that IT plays the following roles in biology:

- IT-aided instruments, such as gene sequencers, DNA microarrays, and microscopes, are used for data collection.
- Large shared, Internet-connected databases, such as gene and protein data banks, allow many researchers to obtain and contribute data to large problems.
- Data analysis methods are used in assembling and searching gene sequences.
- Imaging and visualization, such as Magnetic Resonance Imaging (MRI) and tomography are important in several areas of bioscience.
- Modeling and simulation are used to model protein folding and to help understand complex biological systems such as cells, tissues, organisms, and populations.
- Electronic communication technologies are used to share scientific information and aid scientific collaboration.

## 2. The Review of Related Literature

Although information technology has been used in the biosciences for a long time, the biosciences were initially relatively modest users of IT. A 1966-1967 survey that covered use of computing in the life sciences, found that a lower percentage of life scientists than physical used computers (National Academy of Sciences, 1970). In recent years, however, the use of IT in the biosciences has expanded greatly. Lander et al. (1991) observed that biology had been going through major changes driven by computing for the previous ten years. Since the discovery in the 1950s of how genetic information is coded in DNA, the biosciences have increasingly become much more dependent on IT. Much bioscience research now involves: deciphering the information stored in genetic sequences; understanding how these sequences codes for genes and proteins; and understanding the function and structure of these proteins. In a sense, biology has become driven by the information contained in the genetic code, and information technology is critical in generating and managing this information. The growth in importance of information technology is exemplified by the growth of several new interdisciplinary subfields of biology. One is “bioinformatics,” defined as the application of computers, databases, and computational methods to the management and analysis of biologic information. The human genome project and genome sequencing projects in other organisms, together with new technologies that analyze gene expression patterns, have created vast amounts of data. Bioinformatics has become essential for almost every aspect of data management in modern biology (Kaminski 2000). Another subfield is “computational biology,” which uses mathematical and computational approaches, such as mathematical modeling and computational simulation techniques, to address theoretical and experimental questions in biology. Other new subfields are the ones with the suffix “omics” – which include genomics (the study of the full DNA sequence of organisms, including sequencing, mapping and determining the function of genes); transcriptomics (RNA and gene expression); proteomics (protein expression); metabolomics (metabolites and metabolic networks); pharmacogenomics (how genetics affects individuals responses to drugs); and physiomics (physiological dynamics and functions of whole organisms). Each of these involves the combination of quantitative, experimental, and computational approaches to improve understanding of complex biological systems and processes.

## 3. Method

The scope of this review was defined to be literature limited to English language literature and articles focusing on IT used in the conduct of science and related subjects such as science education.

This study is largely based on a review of literature that describes the uses of IT in bioscience. It sheds light on a somewhat narrower set of questions:

- How has IT been used in the field, and which applications (e.g., modeling and simulation, shared databases, collaborative tools, remote instrumentation) have been most widely used?
- What are some of the major effects and implications, such as the development of new subfields or changes in remote education?

- What are some of the major issues in the uses of IT?

#### 4. Findings and Conclusion

All the literature and the reports bring light to the fact that IT has a substantial impact on biology. Information technology plays three following impacts in biological sciences: IT makes a great revolution in remote education; IT leads to a remarkable improvement in biological simulation; and last but not least Information Technology makes a visible in laboratory studies.

The review shows blatantly that IT is used in a wide variety of applications in bioscience. These applications include automated data collection, statistical analysis of data, Internet-accessible shared databases, modeling and simulation, imaging and visualization of data and analysis, Internet-based communication among scientists, and electronic dissemination of research results.

Another role played by IT is that throughout the scientific cycle in biology. IT is used in many ways throughout the scientific process. This distinguishes IT from most other kinds of scientific equipment, such as microscopes or physics accelerators, which are generally used in one stage of the scientific process, such as data collection. IT aids in hypothesis formation, research design, data collection, data analysis, and communications of scientific results. Table 5 shows the relation of IT to stages of the scientific process. IT is especially important in bioinformatics and the "omics" -- (genomics, proteomics, transcriptomics, etc.). In the geosciences, IT is especially important in analyzing subsurface formations, mapping, and modeling complex systems. There appear to be few, if any, fields that are untouched by IT. Shared Internet accessible databases are important in paleontology; and models and databases are important in population biology and ecology; and genomics are influencing many fields in biology.

There are some systems that are too intricate to study without advanced computational tools for managing and integrating the data into mechanistic models (Department of Energy, 2001). Systems biology aims to model and simulate various systems and visualize the results to help better understand living processes. Instead of the data driven approach of genomics, research in biological systems can be characterized as "model-driven" (Yao, 2002). The complexity of biological systems and the explosion of the quantity of biological information that is rapidly becoming available from experimental and clinical studies require the use of mathematical and computational modeling (Mehr, 2001). Modeling requires taking knowledge in the form of qualitative biological theories and expressing it as explicitly and quantitatively as possible. It requires that implicit knowledge be made explicit so that disparate human knowledge can accumulate in an integrated way (Yao, 2002). Model building also helps point out areas where knowledge is lacking, such as unknown pathways and parameters. Simulation can identify missing components and suggest experiments to gather missing information.

The number of activities that apply information technology to model activity at the cellular and sub cellular levels is on the rise and wide variety. Work is intended to produce both fundamental advances in science as well as practical applications in medicine and agriculture. This work is expected to eventually enable the drawing of the entire metabolic map of a cell.

Computer-aided algorithms are being used to analyze the behavior of thousands of genes at a time and are creating a foundation of data for building integrated models of cellular processes (Schilling et. al 1999 and Kao 1999). Gene expression is regulated through networks of interactions between DNA, RNA, proteins, and small molecules. Because most genetic regulatory networks involve many components connected through interlocking positive and negative feedback loops, it is difficult to obtain an intuitive understanding of their dynamics. Formal methods and computer tools for the modeling and simulation of genetic regulatory networks are needed to understand their operation. Although past attempts to model cellular processes have been disappointing, increases in biological understanding combined with advances in computational methods and in computer power make it possible to foresee construction of useful and predictive simulations of cellular processes (Endy and Brent 2001, Covert et. al. 2001).

There are other uses of IT in biology too. For instance, another cross-cutting area at the intersection of IT and bioscience is the application of artificial intelligence to biology. Molecular biologists and computer scientists have experimented with various computational methods developed in artificial intelligence, including knowledge-based and expert systems, qualitative simulation, and artificial neural networks and other automated learning techniques

(Rawlings and Fox 1994). These methods have been applied to problems in data analysis, construction of databases with advanced retrieval capabilities, and modeling of biological systems. Practical results have been obtained in identifying active genes in genomic sequences, assembling physical and genetic maps, and predicting protein structure.

To sum up, IT has proved to be of conspicuously great impacts on different areas of bioscience and the uses will be on the rise both in new areas and new perspectives.

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